

In the Claims:

1. (Canceled)
2. (Original) A plant nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising:
 - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5; or
 - b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6 by back translation; or
 - c) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 69% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 69% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 63% identity with SEQ ID NO:5; or
 - d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 73% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 73% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 72% identity with SEQ ID NO:6 by back translation.
3. (Currently Amended) A polypeptide with the biological activity of a sucrose-6-phosphate phosphatase as target for herbicides encoded by a nucleic acid molecular sequence as claimed in claim 2.

4. (Currently Amended) A method for detecting functional analogs of SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5, comprising
 - a) [[by]] preparing a probe and subsequently screening a genomic library or cDNA library of the species in question; or
 - b) [[by]] conducting a computer search for analogous sequences in electronic databases.
5. (Currently Amended) An expression cassette comprising
[[a]] genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 2, ~~or~~
 - b) ~~additional functional elements~~; ~~or~~
 - c) ~~a combination of a) and b)~~.
6. (Original) A vector comprising an expression cassette as claimed in claim 5.
7. (Original) A nonhuman transgenic organism comprising at least one nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase as claimed in claim 2, an expression cassette as claimed in claim 5 or a vector as claimed in claim 6 selected from among bacteria, yeasts, fungi, animal cells or plant cells.
8. (Canceled)
9. (Currently Amended) A method of identifying herbicidally active substances, comprising ~~the following steps~~:
 - i. bringing a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase encoded by a nucleic acid sequence comprising
 - a) a nucleic acid sequence as claimed in claim 2;
 - b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation;

into contact with one or more test compounds under conditions which permit the test compound(s) to bind to the nucleic acid molecule or to sucrose-6-phosphate phosphatase; and

ii. detecting whether the test compound binds to the sucrose-6-phosphate phosphatase of i);

or

iii. detecting whether the test compound reduces or blocks the activity of the sucrose-6-phosphate phosphatase of i); or

iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the sucrose-6-phosphate phosphatase of i).

10. (Original) A method as claimed in claim 9, which comprises

i. either expressing, in a transgenic organism, sucrose-6-phosphate phosphatase encoded by a nucleic acid sequence comprising

a) a nucleic acid sequence as claimed in claim 2;

b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation;

or culturing an organism which naturally contains sucrose-6-phosphate phosphatase;

ii. bringing the sucrose-6-phosphate phosphatase of step i) in the cell digest of the transgenic or nontransgenic organism, in partially or homogeneously purified form, into contact with a test compound; and

iii. selecting a test compound which reduces or blocks the activity of the sucrose-6-phosphate phosphatase of step a), where the activity of the sucrose-6-phosphate phosphatase incubated with the test compound is compared with the activity of a sucrose-6-phosphate phosphatase which has not been incubated with a test compound.

11. (Original) A method as claimed in claim 10, wherein, in step iii), the activity is determined by employing sucrose-6-phosphate as substrate and the orthophosphate which is formed in the reaction is determined quantitatively by means of ammonium molybdate.

12. (Currently Amended) A method as claimed in claim 9, ~~which comprises the following steps further comprising:~~

i. ~~generation of~~ generating a transgenic organism as claimed in claim 7 or [[of]] a transgenic organism comprising a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising

b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation; where the polypeptide with the biological activity of a sucrose-6-phosphate phosphatase is overexpressed in the transgenic organism; and

ii. applying a test substance to the transgenic organism of i) and to a nontransgenic organism of the same genotype; and

iii. determining the growth or the viability of the transgenic and the nontransgenic organisms after application of the test substance; and

iv. selection of thereby selecting test substances which bring about reduced growth or reduced viability of the nontransgenic organism in comparison with the growth of the transgenic organism.

13. (Original) A method as claimed in claim 12, which is carried out in a plant organism, a cyanobacterium or a proteobacterium.

14. (Currently Amended) A method for identifying substances with a growth-regulatory action, which comprises the following steps comprising:

- i. ~~generation of~~ generating a transgenic plant comprising a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising
 - a) a nucleic acid sequence as claimed in claim 2; or
 - b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or
 - c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation;where the polypeptide with the biological activity of a sucrose-6-phosphate phosphatase is overexpressed in the transgenic plant;
- ii. applying a test substance to the transgenic plant ~~[[of]] produced in step i)~~ and to a nontransgenic plant of the same genotype;
- iii. determining the growth or the viability of the transgenic and the nontransgenic plants after application of the test substance; and
- iv. ~~selection of~~ thereby selecting test substances which bring about modified growth of the nontransgenic plant in comparison with the growth of the transgenic plant.

15. (Currently Amended) A method as claimed in ~~any of claims 9 to 14~~ claim 9, 10 or 11, wherein the substances are identified in a high-throughput screening.

16. (Canceled)

17. (Currently Amended) A herbicidally active compound identified via one of the methods as claimed in ~~any of claims 9 to 13 and 15~~ claim 9, 10 or 11.

18. (Currently Amended) A growth-regulatory compound identified via the method as claimed in claim 14 ~~or 15~~.

19. (Currently Amended) A process for the preparation of an agrochemical composition, which comprises

a) identifying a herbicidally active compound via one of the methods as claimed in ~~any of claims 9 to 13 and 15~~ claim 9, 10 or 11 ~~or a growth regulatory compound as claimed in claim 14 or 15~~; and

b) formulating [[this]] the herbicidally active compound together with suitable auxiliaries to give herbicidal or growth-regulatory crop protection products.

20. (Currently Amended) A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one compound as claimed in claim 17 ~~or 18 or a composition obtainable via the method mentioned in claim 19~~ to act on plants, their environment and/or on seeds.

21. (Canceled)

22. (Currently Amended) A method for generating nucleic acid sequences which encode a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase, which polypeptide is not inhibited by substances as claimed in claim 17; and which are comprised by a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or a functional equivalent of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5;

which comprises the following process steps:

- a) expressing the protein encoded by the nucleic acid sequence in accordance with i) in a heterologous system or a cell-free system;
- b) performing random or site-directed mutagenesis of the protein by modification of the nucleic acid;
- c) measuring the interaction of the modified gene product with the herbicide;
- d) identifying derivatives of the protein which show less interaction;
- e) assaying the biological activity of the protein after application of the herbicide; and
- f) selecting the nucleic acid sequences which have a modified biological activity against the herbicide.

23. (Currently Amended) A method as claimed in claim 22, wherein the sequences selected in accordance with ~~claim 22 step f~~ are introduced into an organism.

24. A method for generating transgenic plants which are resistant to substances as claimed in claim 17, wherein a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase which comprises

- a) a nucleic acid sequence ~~as claimed in claim 2 with the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5; or~~
- b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6 by back translation; or
- c) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 69% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 69% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 63% identity with SEQ ID NO:5; or
- d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 73%

identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 73% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 72% identity with SEQ ID NO:6 by back translation; or

[[b]] e) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

[[c]] f) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6; is overexpressed in these plants.

25. (Currently Amended) A transgenic plant, ~~generated by a~~ that is the product of the method as claimed in claim 24.